Erratum: mRNA Turnover Rate Limits siRNA and microRNA Efficacy

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ERRATUM

mRNA turnover rate limits siRNA and microRNA efficacy

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Correction to: *Molecular Systems Biology* **6:** 433. doi:10.1038/msb.2010.89; published online 16 November 2010

Since the publication of the above paper, the authors have noticed that the correspondence details for E Larsson were incorrect: Computational Biology Program should have read Computational Biology Center. The correct details are shown above.

The authors also noticed an error in Figure 5. During typesetting, both the dashed vertical line at −1.5 on the *x* axis, used to indicate the threshold for generating the bar graph to the right, and the dashed green curve were moved to the left.

Please see the corrected figure below.

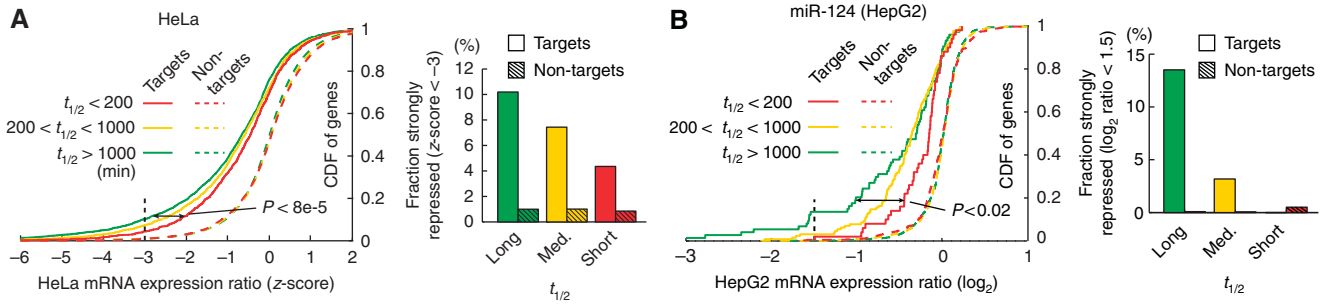

Figure 5 High-turnover mRNAs are less influenced by microRNA overexpression. (**A**) Genes were divided into three bins based on their half-lives ($t_{1/2}$). The plot shows the cumulative distribution function (CDF) of relative mRNA expression levels after transfection of synthetic microRNAs. Z-normalized $\log_2$-transformed mRNA expression ratios from 20 microRNA overexpression experiments were pooled. The bar graphs indicate, for each half-life bin, the fraction of predicted targets or non-targets that were strongly repressed (*z*-score < -3). (**B**) Similar analysis based on a time series of miR-124 overexpression in HepG2 cells. Result shown is for 24 h after transfection. Source data is available for this figure at www.nature.com/msb.

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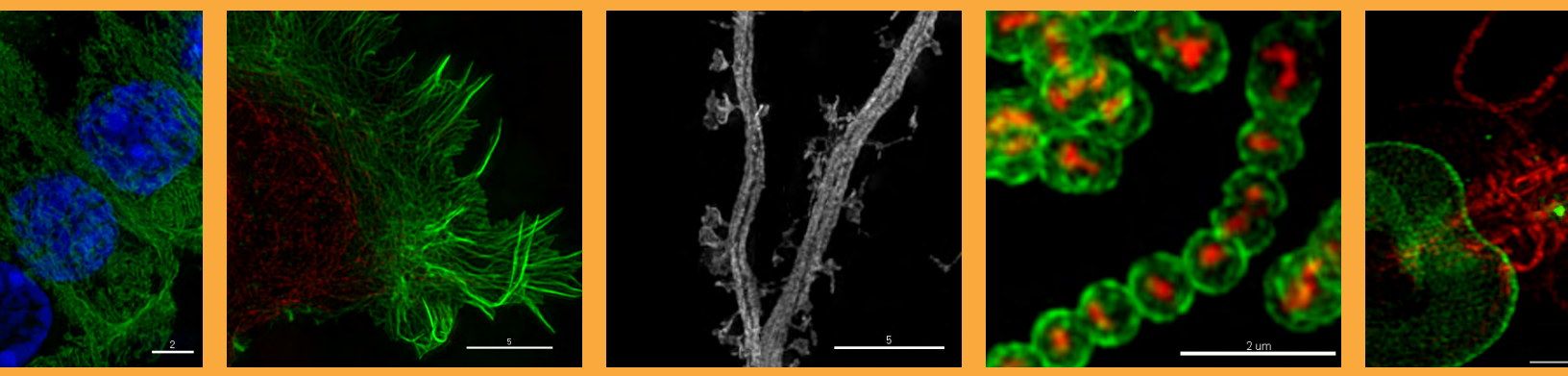

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